IN THE SPECIFICATION:

At page 3, the paragraph encompassing lines 6-18 is amended as follows:

On the other hand, Fas antigen is a membrane protein whose participation in programmed cell death, namely apoptosis has been clearly shown. Yonehara *et al.* have prepared monoclonal antibodies for human cell surface antigens and obtained an anti-Fas antibody showing lethal activity upon various human cells (see *J. Exp. Med.*, 169, 1747 (1989)). cDNA of a cell surface molecule recognizable by the anti-Fas antibody has been isolated, and structure of the human Fas antigen has been determined (SEQ ID NO:22) (see *Cell*, 66, 233 (1991)). This Fas antigen is composed of 335 amino acid residues, and 16 amino acid residues in the N-terminus is assumed to be its signal peptide. A transmembrane region composed of 17 hydrophobic amino acid residues is present in a central position of the molecule, and it is considered that 157 amino acid residues in the N-terminus exist as its extracellular region and the C-terminal side sequence of 145 amino acid residues is its cytoplasmic region.

At page 3, the paragraph encompassing line 19, through page 4, line 4, is amended as follows:

Since the structure of the Fas antigen is resemble in the structure of a receptor for tumor necrosis factor (TNF), it is assumed that the apoptosis of the Fas antigen occurs by a mechanism similar to the action of TNF. Functional regions of the Fas antigen have also been revealed gradually, and it has been found that the region essential for the signal transduction of apoptosis (functional region) is an amino acid sequence of the 175th to 304th positions (see *J. Biol. Chem*, 268, 10932 (1993)). In addition, the amino acid sequence of mouse Fas antigen has also been revealed (SEQ ID NO:23) (see *J. Immunology*, 148, 1274 (1992)), and it has a homology of

B2

49.3% to the human Fas antigen as a whole. It is considered also that its functional region is an amino acid sequence of the 166th to 291st positions corresponding to the region of the human Fas antigen.

At page 15, the paragraph encompassing lines 9-14 is amended as follows:

B3

Regarding the UAS which is a Gal4 protein responsive element contained as a repeating structure in the reporter plasmid of the invention, an already known sequence was used (see (*Cell*, 83, 803 (1995) and *Cell*, 83, 813 (1995)). That is, a sequence in which a sequence of 5' – CGACGGAGTACTGTCCTCCG – 3' (SEQ ID NO:19) is repeated several times, specifically at least three 3 times, preferably 4 times, more preferably 5 times.

At page 25, the paragraph encompassing lines 3-8 is amended as follows:

B4

R6: An antisense primer, 5' – CCTCTAGACTAGCTGGCATAGTCGGGCACGTCGT AGGGGTAGTCGACGTACAAGTCCTTGTAGATCTCC – 3' (SEQ ID NO:12), corresponding to a sequence of Glu^{472} to Tyr^{478}, in which an *Sal*I site, an influenza hemagglutinin epitope (Tyr Pro Tyr Asp Val Pro Asp Tyr Ala) (SEQ ID NO:20) as an epitope tag sequence for use in the detection of expressed protein, a translation termination codon and an *Xba*I site were arranged in this order, was synthesized.

At page 27, the paragraph encompassing lines 6-21 is amended as follows:

B5

An expression vector pTKβ (manufactured by Clontech, Cat. No. 6179-1) under control of herpes simplex virus thymidine kinase (TK) promoter was used. *Not*I sites upstream and downstream of the β–galactosidase structural gene of pTKβ were digested, and both termini are smooth-ended. Next, a DNA encoding the MFas protein, as a DNA to be inserted, was excised from pBSMFas by using restriction enzymes *Hind*III and *Bam*HI and blunt-ended. Both of the

DNAs were ligated to select a clone in which the MFas structural gene was connected to the region downstream of TK promoter in the forward direction. The thus obtained plasmid pTK-MFas of about 4400 bp contains a DNA encoding MFas protein under control of the TK promoter. Next, *Sal*I site located in the region upstream of the TK promoter of plasmid pTK-MFas was digested and blunt-ended, and then a multi-cloning site was inserted as a linker DNA (SEQ ID NO:17, *Eco*RI-*Sal*I-*Kpn*I-*Eco*RV-*Sac*I-*Not*I):

5' – GAATTCGTCGACGGTACCGATATCGAGCTCGCGGCCGC – 3'

3' – CTTAAGCAGCTGCCATGGCTATAGCTCGAGCGCCGGCG – 5' (SEQ ID NO:21)

to obtain pTK-MFas-ML1(5'-*Eco*RI-*Sal*I-*Kpn*I-*Eco*RV-*Sac*I-*Not*I-3').